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RAW SEQUENCE LISTING PATENT APPLICATION US/09/490,187

DATE: 02/15/2000
TIME: 14:57:42

Input Set: I490187.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Chaudhary, Preet M.
2 <120> TITLE OF INVENTION: Gene Expression in Ectodermal Dysplasia
3 <130> FILE REFERENCE: utsd680
4 <140> CURRENT APPLICATION NUMBER: US/09/490,187
5 <141> CURRENT FILING DATE: 2000-01-23
6 <160> NUMBER OF SEQ ID NOS: 2
7 <170> SOFTWARE: PatentIn Ver. 2.1
8 <210> SEQ ID NO 1
9 <211> LENGTH: 1489
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18      Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr
19      1          5          10          15
20      ctt tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa tca 157
21      Leu Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser
22      20          25          30
23      gga gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt 205
24      Gly Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val
25      35          40          45
26      ccc tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc 253
27      Pro Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly
28      50          55          60
29      ttc ggc tat ggg gag gat gca cag tgt gtg gcg tgc cgg ctg cac agg 301
30      Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Ala Cys Arg Leu His Arg
31      65          70          75
32      ttc aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc 349
33      Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys
34      80          85          90          95
35      gca gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat 397
36      Ala Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp
37      100          105          110
38      gcc atc tgc ggg gac tgc ttg cca gga ttt tat agg aag acg aaa ctt 445
39      Ala Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu
40      115          120          125
41      gtc ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct 493
42      Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro
43      130          135          140
44      cct tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg 541

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49	160					165					170					175	
50	agc	gct	ctg	gcc	acc	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	637
51	Ser	Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	
52					180					185					190		
53	tat	tgt	aag	aga	cag	ttt	atg	gaa	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	685
54	Tyr	Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	
55				195					200					205			
56	tca	cag	gac	att	cag	tac	aac	gag	act	gag	ctg	tgc	tgt	ttt	gac	aga	733
57	Ser	Gln	Asp	Ile	Gln	Tyr	Asn	Glu	Thr	Glu	Leu	Ser	Cys	Phe	Asp	Arg	
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63	Asp	Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	
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66	Cys	Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	
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69	His	Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	
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72	Met	Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	
73		290					295					300					
74	ttt	tca	gat	gcc	tgg	cct	ctg	atg	cag	aat	ccc	atg	ggg	ggg	gac	aac	1021
75	Phe	Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	
76	305					310					315						
77	atc	tct	ttt	tgt	gac	tct	tat	cct	gaa	ctc	act	gga	gaa	gac	att	cgt	1069
78	Ile	Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	
79	320				325					330					335		
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84	Ser	Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	
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86	aac	ttt	aca	gca	gct	act	gat	tta	tct	aga	tat	aac	aac	aca	ctg	gta	1213
87	Asn	Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	
88		370					375					380					
89	gaa	tca	gca	tca	act	cag	gat	gca	cta	act	atg	aga	agc	cag	cta	gat	1261
90	Glu	Ser	Ala	Ser	Thr	Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	
91		385				390					395						
92	cag	gag	agt	ggc	gct	gtc	atc	cac	cca	gcc	act	cag	acg	tcc	ctc	cag	1309
93	Gln	Glu	Ser	Gly	Ala	Val	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	
94	400				405				410					415			

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111     35 40 45
112     Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
113     50 55 60
114     Gly Tyr Gly Glu Asp Ala Gln Cys Val Ala Cys Arg Leu His Arg Phe
115     65 70 75 80
116     Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
117     85 90 95
118     Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
119     100 105 110
120     Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
121     115 120 125
122     Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
123     130 135 140
124     Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
125     145 150 155 160
126     Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
127     165 170 175
128     Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
129     180 185 190
130     Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
131     195 200 205
132     Gln Asp Ile Gln Tyr Asn Glu Thr Glu Leu Ser Cys Phe Asp Arg Pro
133     210 215 220
134     Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
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137     245 250 255
138     Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
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141     275 280 285
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156	Glu Ser Gly Ala Val Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val			
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158	Arg Gln Arg Leu Gly Ser Leu			
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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
